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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: Thu Sep 13 18:24:01 EDT 2007

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Application No: 10580813 Version No: 1.0

Input Set:

Output Set:

Started: 2007-09-04 13:46:13.598
Finished: 2007-09-04 13:46:14.532
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 934 ms
Total Warnings: 11
Total Errors: 0
No. of SeqIDs Defined: 11
Actual SeqID Count: 11

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (3)
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W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
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SEQUENCE LISTING

<110> Max Planck Gesellschaft zur Foerderung der Wissensc

<120> Substance binding human IgG Fc receptor IIb (Fc gamma
RIIb)

<130> 30287P_WO HC

<140> 10580813

<141> 2007-09-04

<150> PCT/EP2004/013450

<151> 2004-11-26

<150> EP03027000.3

<151> 2003-11-26

<160> 11

<170> PatentIn Ver. 2.1

<210> 1

<211> 172

<212> PRT

<213> human

<220>

<223> Fc gamma RIIa

<400> 1

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Leu	Gln	Glu	Asp	Ser	Val	Thr	Leu	Thr	Cys	Gln	Gly	Ala	Arg	Ser	Pro
			20					25					30		

Glu	Ser	Asp	Ser	Ile	Gln	Trp	Phe	His	Asn	Gly	Asn	Leu	Ile	Pro	Thr
		35					40					45			

His	Thr	Gln	Pro	Ser	Tyr	Arg	Phe	Lys	Ala	Asn	Asn	Asn	Asp	Ser	Gly
	50						55				60				

Glu	Tyr	Thr	Cys	Gln	Thr	Gly	Gln	Thr	Ser	Leu	Ser	Asp	Pro	Val	His
65				70						75				80	

Leu	Thr	Val	Leu	Ser	Glu	Trp	Leu	Val	Leu	Gln	Thr	Pro	His	Leu	Glu
			85					90						95	

Phe	Gln	Glu	Gly	Glu	Thr	Ile	Met	Leu	Arg	Cys	His	Ser	Trp	Lys	Asp
		100						105					110		

Lys	Pro	Leu	Val	Lys	Val	Thr	Phe	Phe	Gln	Asn	Gly	Lys	Ser	Gln	Lys
		115					120					125			

Phe	Ser	Arg	Leu	Asp	Pro	Thr	Phe	Ser	Ile	Pro	Gln	Ala	Asn	His	Ser
130						135					140				

His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe
145 150 155 160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro
165 170

<210> 2

<211> 172

<212> PRT

<213> human

<220>

<223> Fc gamma RIIB

<400> 2

Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Gln Trp Ile Asn Val
1 5 10 15

Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Arg Gly Thr His Ser Pro
20 25 30

Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
35 40 45

His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
50 55 60

Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
65 70 75 80

Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
85 90 95

Phe Gln Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser Trp Lys Asp
100 105 110

Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Lys Lys
115 120 125

Phe Ser Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala Asn His Ser
130 135 140

His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Tyr
145 150 155 160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro
165 170

<210> 3

<211> 13

<212> PRT

<213> human

<220>

<223> glycopeptide CDE [126-137]

<400> 3

Ser Lys Lys Phe Ser Arg Ser Asp Pro Asn Phe Ser Gly
1 5 10

<210> 4

<211> 312

<212> DNA

<213> Unknown Organism

<220>

<221> CDS

<222> (1)..(312)

<223> variable light region of mAb GB3

<220>

<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 4

aga att cag ctg acc cag tct cca tcc tcc tta tct gcc tct ctg gga 48
Arg Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

gaa aga gtc agt ctc act tgt cgg gca agt cag gaa att agt ggt tac 96
Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
20 25 30

tta agc tgg ctt cag cag aaa cca gat gga act att aaa cgc ctg atc 144
Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile
35 40 45

tac gcc aca tcc gct tta gat tct ggt gtc cca aaa agg ttc agt ggc 192
Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
50 55 60

agt ggg tct ggg tca aat tat tct ctc acc atc agc agc ctt gag tct 240
Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

gaa gat ttt gca gac tat tac tgt cta caa tat gct aat tat ccg tac 288
Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr
85 90 95

acg ttc gga ggg ggg acc aag ctg 312
Thr Phe Gly Gly Gly Thr Lys Leu
100

<210> 5

<211> 104

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 5

Arg Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
20 25 30

Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile
35 40 45

Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu
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<210> 6

<211> 312

<212> DNA

<213> Unknown Organism

<220>

<221> CDS

<222> (1)..(312)

<223> variable heavy region of mAb GB3

<220>

<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 6

gtg cag ctg cag cag tct gga cct gag ctg gtg aag cct ggg gct tca 48
Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
1 5 10 15

gtg aag att tcc tgc aag gct tct ggc tac acc ttc act gac tac tat 96
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
20 25 30

ata tac tgg gtg aaa cag tgg cct gga cag gga ctt gag tgg att gga 144
Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
35 40 45

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tgg att ttt cct gga act ggt aat act tac tac aat gaa aac ttc aag 192
Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
    50                55                60

gac aag gcc aca ctt act ata gat aga tcc tcc agc aca gcc tac atg 240
Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met
    65                70                75                80

ttg ctc ggc agc ctg acc tct gag gac tct gcg gtc tat ttc tgt tat 288
Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr
                85                90                95

ggg ccc ttt gct tac tgg ggc caa 312
Gly Pro Phe Ala Tyr Trp Gly Gln
    100

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<210> 7

<211> 104

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 7

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Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
    1                5                10                15

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Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
                20                25                30

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Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
    35                40                45

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Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
    50                55                60

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Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met
    65                70                75                80

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Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr
                85                90                95

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Gly Pro Phe Ala Tyr Trp Gly Gln
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<210> 8

<211> 309

<212> DNA

<213> Unknown Organism

<220>

<221> CDS

<222> (1)..(309)

<223> variable light region of mAb CE5

<220>

<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 8

gag ctc acc cag tct cca gcc tcc ctt tct gcg tct gtg gga gaa act 48
Glu Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly Glu Thr
1 5 10 15

gtc acc atc aca tgt cga gca agt ggg aat att cac aat tat tta gca 96
Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
20 25 30

tgg tat cag cag aaa cag gga aaa tct cct cag ctc ctg gtc tat tat 144
Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr Tyr
35 40 45

aca aca acc tta gca gat ggt gtg cca tca agg ttc agt ggc agt gga 192
Thr Thr Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
50 55 60

tca gga aca caa tat tct ctc aag atc aac agc ctg caa cct gaa gat 240
Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp
65 70 75 80

ttt ggg agt tat tac tgt caa cat ttt tgg agt act cct cgg acg ttc 288
Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Arg Thr Phe
85 90 95

ggt gga ggg acc aag ctc gag 309
Gly Gly Gly Thr Lys Leu Glu
100

<210> 9

<211> 103

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 9

Glu Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly Glu Thr
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr Leu Ala
20 25 30

Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val Tyr Tyr
35 40 45

Thr Thr Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly Ser Gly

50

55

60

Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Arg Thr Phe
85 90 95

Gly Gly Gly Thr Lys Leu Glu
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<210> 10

<211> 339

<212> DNA

<213> Unknown Organism

<220>

<221> CDS

<222> (3)..(338)

<223> variable heavy region of mAb CE5

<220>

<223> Description of Unknown Organism: sequence
comprised by an antibody

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tg cag gag tca gga cct ggc ctg gtg gcg ccc tca cag agc ctg tcc 47
Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
1 5 10 15

atc aca tgc acc gtc tca ggg ttc tca tta acc ggc tat ggt gta aac 95
Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn
20 25 30

tgg gtt cgc cag cct cca gga aag ggt ctg gag tgg ctg gga atg att 143
Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile
35 40 45

tgg ggt gat gga aac aca gac tat aat tca gct ctc aaa tcc aga ctg 191
Trp Gly Asp Gly Asn Thr Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu
50 55 60

agc atc agc aag gac aac tcc aag agc caa gtt ttc tta aaa atg aac 239
Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
65 70 75

agt ctg cac act gat gac aca gcc agg tac tac tgt gcc aga gag aga 287
Ser Leu His Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Glu Arg
80 85 90 95

gat tat agg ctt gac tac tgg ggc caa ggg acc acg gtc acc gtc tcc 335
Asp Tyr Arg Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser
100 105 110

tca g 339

Ser

<210> 11

<211> 112

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 11

Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Ile
1 5 10 15

Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn Trp
20 25 30

Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile Trp
35 40 45

Gly Asp Gly Asn Thr Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu Ser
50 55 60

Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser
65 70 75 80

Leu His Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Glu Arg Asp
85 90 95

Tyr Arg Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
100 105 110